

What is claimed is:

1. A nucleic acid molecule, comprising a nucleotide sequence that:
  - a) comprises a moiety binding region; and
  - b) encodes an interacting domain,wherein said interacting domain directly or indirectly binds with said moiety binding region.
2. The nucleic acid molecule of claim 1, wherein said nucleic acid molecule comprises ssRNA or dsRNA.
3. The nucleic acid molecule of claim 2, further comprising or encoding at least one random sequence or at least one sequence of interest.
4. The nucleic acid molecule of claim 1, wherein said nucleic acid molecule comprises ssDNA.
5. The nucleic acid molecule of claim 4, further comprising or encoding at least one random sequence or at least one sequence of interest.
6. The nucleic acid molecule of claim 1, wherein said nucleic acid molecule comprises dsDNA.
7. The nucleic acid molecule of claim 6, further comprising or encoding at least one random sequence or at least one sequence of interest.
8. The nucleic acid molecule of claim 1, further comprising or encoding a spacer region.

9. The nucleic acid molecule of claim 8, wherein said spacer region comprises or encodes at least one purification domain or at least one detection domain.
10. The nucleic acid molecule of claim 1, further comprising or encoding at least one expression control sequence.
11. The nucleic acid molecule of claim 1, further comprising or encoding at least one start codon.
12. A vector comprising the nucleic acid molecule of one of claims 1, 2, 4 or 6.
13. A vector comprising the nucleic acid molecule of one of claims 3, 5 or 7.
14. The vector of one of claims 12 or 13, wherein said vector is selected from the group consisting of a viral vector, a plasmid, a phage, a liposome, a microsphere or a linear dsDNA molecule.
15. The nucleic acid molecule of one of claims 1, 2, 4 or 6, wherein said nucleic acid molecule is operably linked to said interacting domain.
16. The nucleic acid molecule of one of claims 3, 5 or 7, wherein said nucleic acid molecule is operably linked to said interacting domain.
17. The nucleic acid molecule of one of claims 15 or 16, wherein said interacting domain binds directly or indirectly with said moiety binding region.
18. The nucleic acid molecule of one of claims 2 or 3, wherein said nucleic acid molecule is operably linked to said interacting domain.

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19. The nucleic acid molecule of one of claims 3, 5 or 7 wherein said nucleic acid molecule is operably linked to a polypeptide encoded by said random sequence or said sequence of interest.
20. The nucleic acid molecule of claim 18, wherein said nucleic acid molecule is substantially devoid or devoid of ribosomes.
21. The nucleic acid molecule of one of claims 1, 2, 3, 4, 5, 6 or 7, wherein said moiety binding region is substantially free of secondary structure.
22. The nucleic acid molecule of one of claims 3, 5 or 7, wherein said moiety binding region is substantially free of secondary structure.
23. The nucleic acid molecule of any one of claims 21 or 22, wherein said moiety binding region directly or indirectly reduces the efficiency of translation of said nucleic acid molecule.
24. The nucleic acid molecule of one of claims 1, 2, 3, 4, 5, 6 or 7, wherein said moiety binding region comprises at least one secondary structure.
25. The nucleic acid molecule of one of claims 3, 5 or 7, wherein said moiety binding region comprises at least one secondary structure.
26. The nucleic acid molecule of one of claims 22, 23, 24 or 25, wherein said at least one secondary structure is a stem-loop configuration or a hairpin configuration or wherein two stretches of complementary sequences are in one nucleic acid molecule.

27. The nucleic acid molecule of one of claims 24, 25 or 26, wherein said secondary structure is within between about 60 nucleotides and about 2 nucleotides of a start codon, within between about 50 nucleotides and about 4 nucleotides of a start codon, within between about 40 nucleotides and about 6 nucleotides of a start codon, within between about 30 nucleotides and about 8 nucleotides of a start codon or within between about 20 nucleotides and about 10 nucleotides of a start codon.
28. The nucleic acid molecule of one of claims 24, 25, 26 or 27 wherein said secondary structure directly or indirectly reduces the efficiency of translation of said nucleic acid molecule, optionally by the pairing of said two stretches of complementary sequences are in one nucleic acid molecule..
29. The nucleic acid molecule of one of claims 15, 16, 17 or 18, wherein said moiety binding region binds with said interacting domain to form a moiety binding region/interacting domain complex.
30. The nucleic acid molecule of claim 16, wherein said moiety binding region is operably linked to said interacting domain to form a moiety binding region/interacting domain complex.
31. The nucleic acid molecule of any one of claims 29 or 30, wherein said moiety binding region/interacting domain complex reduces the efficiency of translation of said nucleic acid molecule.
32. The nucleic acid molecule of any one of claims 29 or 30, wherein said interacting domain comprises a polypeptide.

33. The nucleic acid molecule of one of claims 15, 16, 17 or 18, wherein said polypeptide encoded by said random sequence is bound with a substance of interest.
- 5 34. The nucleic acid molecule of claim 33, wherein said substance of interest is on a solid support.
35. The nucleic acid molecule of claim 33, wherein said substance of interest is on or within a cell.
- 10 36. The nucleic acid molecule of claim 35, wherein said cell is *ex vivo*.
37. The nucleic acid molecule of claim 35, wherein said cell is *in vivo* in a subject.
- 15 38. The nucleic acid molecule of claim 35, wherein said cell is a normal cell or an abnormal cell.
39. The nucleic acid molecule of claim 38, wherein said abnormal cell is a neoplastic cell or a virus infected cell.
- 20 40. The nucleic acid molecule of claim 33, wherein said substance of interest is on or within an etiological agent.
- 25 41. The nucleic acid molecule of claim 40, wherein said etiological agent is selected from the group consisting of a bacteria, a spore, a virus, a parasite or a prion.

42. The nucleic acid molecule of claim 33, wherein said substance of interest comprises at least one organic molecule, an inorganic molecule, a polymer, a polypeptide, a nucleic acid molecule, a ribozyme, a lipid, a carbohydrate, a small molecule, a biomacromolecule or a drug.
43. A library of nucleic acid molecules of one of claims 3, 5 or 7.
44. The library of nucleic acid molecules of claim 43, wherein said library comprises at least two different random sequences, at least two different sequences of interest or a combination of at least one random sequence and at least one sequence of interest.
45. A library of nucleic acid molecules of claim 16.
46. The library of nucleic acid molecules of claim 45, wherein said library comprises at least two different random sequences, at least two different sequences of interest or a combination of at least one random sequence and at least one sequence of interest.
47. A library of nucleic acid molecules of one of claims 19 or 20.
48. The library of nucleic acid molecules of claim 47, wherein said library comprises at least two different random sequences, at least two different sequences of interest or a combination of at least one random sequence and at least one sequence of interest.
49. A library of nucleic acid molecules of one of claims 21 or 25.

50. The library of nucleic acid molecules of claim 49, wherein said library comprises at least two different random sequences, at least two different sequences of interest or a combination of at least one random sequence and at least one sequence of interest.
51. A library of nucleic acid molecules of claim 30.
52. The library of nucleic acid molecules of claim 51, wherein said library comprises at least two different random sequences, at least two different sequences of interest or a combination of at least one random sequence and at least one sequence of interest.
53. The library of nucleic acid molecules of any one of claims 42 to 55, wherein said library is contacted with at least one substance of interest.
54. The library of nucleic acid molecules of claim 53, wherein said at least one substance of interest is directly or indirectly bound on a solid support or in solution.
55. The nucleic acid molecule of claim 53, wherein said substance of interest is on or within a cell.
56. The nucleic acid molecule of claim 55, wherein said cell is *ex vivo*.
57. The nucleic acid molecule of claim 55, wherein said cell is *in vivo* in a subject.
58. The nucleic acid molecule of claim 55, wherein said cell is a normal cell or an abnormal cell.

59. The nucleic acid molecule of claim 58, wherein said abnormal cell is a neoplastic cell or a virus infected cell.
- 5 60. The nucleic acid molecule of claim 53, wherein said substance of interest is on or within an etiological agent.
61. The nucleic acid molecule of claim 60, wherein said etiological agent is selected from the group consisting of a bacteria, a virus, a parasite or a prion.
- 10 62. A library of vectors of one of claims 12, 13 or 14.
63. A method for identifying a nucleic acid molecule or sequence, comprising:
1. providing at least one nucleic acid molecule of claim 3 or claim 5;
  2. translating said nucleic acid molecule to provide at least one complex, wherein said complex comprises a polypeptide operably linked to a random sequence or a nucleic acid sequence or a nucleic acid molecule of interest;
  3. contacting said at least one complex with at least one substance of interest;
  4. selecting at least one complex that binds with said at least one substance of interest; and
  5. identifying said random sequence or said nucleic acid sequence of interest or nucleic acid molecule of interest.
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- 25 64. The method of claim 63, wherein said contacting comprises conditions that promote binding of said complex to said substance of interest.



65. The method of claim 63, wherein said identifying comprising amplifying said random sequence or said nucleic acid sequence of interest or said nucleic acid molecule of interest.
- 5 66. The method of claim 63, wherein said substance of interest is on a solid support or in solution.
67. The method of claim 63, wherein said substance of interest is on or within a cell.
- 10 68. The method of claim 63, wherein said substance of interest is on or within an etiological agent.
69. A nucleic acid molecule comprising a random sequence or nucleic acid sequence or nucleic acid molecule identified by the method of claim 63.
- 15 70. The method of claim 63, further comprising the step of sequencing the identified random sequence or nucleic acid sequence of interest or said nucleic acid molecule of interest.
- 20 71. The method of claim 63, further comprising performing steps 1, 2, 3 and 4 reiteratively.
72. The method of claim 63, further comprising performing steps 1, 2, 3, 4 and 5 reiteratively.
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73. A method for identifying a nucleic acid molecule or sequence, comprising:
1. providing at least one nucleic acid molecule of one of claims 5 or 7;
  2. transcribing said nucleic acid molecule to a corresponding RNA molecule;
  3. translating said RNA molecule to provide at least one complex, wherein said complex comprises a polypeptide operably linked to a random sequence or a nucleic acid sequence of interest or a nucleic acid molecule of interest;
  4. contacting said at least one complex with at least one substance of interest;
  5. selecting at least one complex that binds with said at least one substance of interest; and
  6. identifying said random sequence or nucleic acid sequence of interest or nucleic acid molecule of interest.
74. The method of claim 73, wherein said contacting comprises conditions that promote binding of said complex to said substance of interest.
75. The method of claim 73, wherein said identifying comprising amplifying said random sequence or nucleic acid sequence of interest or nucleic acid molecule of interest.
76. The method of claim 73, wherein said substance of interest is on a solid support or in solution.
77. The method of claim 73, wherein said substance of interest is on or within a cell.

78. The method of claim 73, wherein said substance of interest is on or within an etiological agent.
79. A nucleic acid molecule comprising a random sequence or nucleic acid sequence or nucleic acid molecule identified by the method of claim 73.
80. The method of claim 73, further comprising the step of sequencing the identified random sequence or nucleic acid sequence of interest or said nucleic acid molecule of interest.
81. The method of claim 73, further comprising performing steps 1, 2, 3 and 4 iteratively.
82. The method of claim 73, further comprising performing steps 1, 2, 3, 4 and 5 iteratively.
83. The method of claim 73, further comprising performing steps 1, 2, 3, 4, 5 and 6 iteratively.

84. A method for identifying a polypeptide encoded by a random nucleic acid sequence or nucleic acid sequence of interest or nucleic acid molecule of interest, comprising:
1. providing at least one nucleic acid molecule of claim 3 or 5;
  2. translating said nucleic acid molecule to provide at least one complex, wherein said complex comprises a polypeptide operably linked to a random sequence or a nucleic acid sequence of interest or a nucleic acid molecule of interest;
  3. contacting said at least one complex with at least one substance of interest;
  4. selecting at least one complex that binds with said at least one substance of interest; and
  5. identifying said polypeptide in said complex.
85. The method of claim 84, wherein said contacting comprises conditions that promote binding of said transcript to said substance of interest.
86. The method of claim 84, wherein said identifying comprises amplifying said random sequence or nucleic acid sequence of interest or nucleic acid molecule of interest or nucleic acid molecule of interest.
87. The method of claim 84, wherein said substance of interest is on a solid support or in solution.
88. The method of claim 84, wherein said substance of interest is on or within a cell.
89. The method of claim 84, wherein said substance of interest is on or within an etiological agent.

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90. A polypeptide identified by the method of claim 84.
91. The method of claim 84, further comprising the step of sequencing said identified polypeptide.
92. The method of claim 84, further comprising performing steps 1, 2, 3 and 4 iteratively.
- 10 93. The method of claim 84, further comprising performing steps 1, 2, 3, 4 and 5 iteratively.
- 15 94. A method for identifying a polypeptide encoded by a random nucleic acid sequence or nucleic acid sequence of interest or nucleic acid molecule of interest in the nucleic acid, comprising:
1. providing at least one nucleic acid molecule of one of claims 5 or 7;
  2. transcribing said nucleic acid molecule to a corresponding RNA molecule;
  - 20 3. translating said RNA molecule to provide at least one complex, wherein said complex comprises a polypeptide operably linked to a random sequence or a nucleic acid sequence of interest or a nucleic acid molecule of interest;
  4. contacting said at least one complex with at least one substance of interest;
  - 25 5. selecting at least one complex that binds with said at least one substance of interest; and
  6. identifying said polypeptide in said complex.

95. The method of claim 94, wherein said contacting comprises conditions that promote binding of said transcript to said substance of interest.
96. The method of claim 94, wherein said identifying comprising amplifying said random sequence or nucleic acid sequence of interest or nucleic acid molecule of interest or nucleic acid molecule of interest.
97. The method of claim 94, wherein said substance of interest is on a solid support or in solution.
98. The method of claim 94, wherein said substance of interest is on or within a cell.
99. The method of claim 94, wherein said substance of interest is on or within an etiological agent.
100. A polypeptide identified by the method of claim 94.
101. The method of claim 94, further comprising the step of sequencing the identified polypeptide.
102. The method of claim 94, further comprising performing steps 1, 2, 3 and 4 reiteratively.
103. The method of claim 94, further comprising performing steps 1, 2, 3, 4 and 5 reiteratively.
104. The method of claim 94, further comprising performing steps 1, 2, 3, 4, 5 and 6 reiteratively.

105. A method for identifying a test compound, comprising:
- a) contacting a target with a complex that:
    - 1) comprises a moiety binding region;
    - 2) encodes an interacting domain; and
    - 3) comprises a random sequence or a sequence of interest that encodes a polypeptide;wherein said interacting domain directly or indirectly binds with said moiety binding region;
  - b) identifying polypeptides bound with said target;
  - c) determining the structure of said polypeptide; and
  - d) identifying moieties that have structures that have space filling shapes that are similar to at least a portion of said polypeptide.
106. A test compound identified by method of claim 105.
107. A pharmaceutical composition identified by a method of claim 105.
108. A method for identifying a target, comprising:
- a) contacting a substance of interest with a complex that:
    - 1) comprises a moiety binding region;
    - 2) encodes an interacting domain; and
    - 3) comprises a random sequence or a sequence of interest that encodes a polypeptide;wherein said interacting domain directly or indirectly binds with said moiety binding region;
  - b) identifying targets that bind with said complex.
109. A target identified by the method of claim 108.

110. A pharmaceutical target ~~identified~~ by the method of claim 108.

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